

Engineering Conferences International ECI Digital Archives

Cell Culture Engineering XV

Proceedings

Spring 5-10-2016

Real time prediction and control of glycoform profile of mammalian cell cultures using in silicoglycosylation model coupled with extracellular metabolites

Sha Sha

University of Massachusetts at Lowell

Seongkyu Yoon

University of Massachusetts at Lowell

Follow this and additional works at: http://dc.engconfintl.org/cellculture_xv



Part of the [Biomedical Engineering and Bioengineering Commons](#)

Recommended Citation

Sha Sha and Seongkyu Yoon, "Real time prediction and control of glycoform profile of mammalian cell cultures using in silicoglycosylation model coupled with extracellular metabolites" in "Cell Culture Engineering XV", Robert Kiss, Genentech Sarah Harcum, Clemson University Jeff Chalmers, Ohio State University Eds, ECI Symposium Series, (2016). http://dc.engconfintl.org/cellculture_xv/119

This Abstract is brought to you for free and open access by the Proceedings at ECI Digital Archives. It has been accepted for inclusion in Cell Culture Engineering XV by an authorized administrator of ECI Digital Archives. For more information, please contact franco@bepress.com.

Realtime prediction and control of glycoform profile of mammalian cell cultures using *in silico* glycosylation model coupled with extracellular metabolites

Sha Sha and Seongkyu Yoon

Department of Chemical Engineering, University of Massachusetts Lowell, MA, USA

Abstract

In silico mechanistic models for glycosylation are investigated for biotherapeutics development and production. The models systematically describe the transport-kinetics of glycosylation process and serve as a prediction framework for glycan profile. However, inputs for those models are generally limited to intracellular parameters, such as enzymatic activity and nucleotide sugar concentration. These intracellular metabolites are unfortunately inaccessible in process. To modulate those models for glycoform prediction in culture process, linkage between measurable culture variations and the intracellular metabolites change will be thoroughly investigated. The measurable metabolites and intracellular variables associated with *in silico* glycosylation model are integrated in the modeling. Despite a few efforts, the mechanism of nucleotide sugar synthesis is not being fully understood and the accuracy of linking model is not at practical level. Here we propose development of mathematical models bridging in-process extracellular metabolites and variation of intracellular glycosylation related metabolites with experimental validation. In order to assess the model robustness, in-process extracellular and intracellular metabolites are generated via a few feeding strategy study with mammalian CHO cell cultures.